

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number:

10/530,340

Source:

PCT

Date Processed by STIC:

4-13-05

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RAW SEQUENCE LISTING

DATE: 04/13/2005

PATENT APPLICATION: US/10/530,340

TIME: 09:40:13

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\04132005\J530340.raw

3 <110> APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
 4 REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
 5 HUMAN SERVICES
 6 Tsai, Robert Y.L.
 7 McKay, Ronald D.G.
 9 <120> TITLE OF INVENTION: METHODS FOR CONTROLLING PROLIFERATION OF CELLS
 11 <130> FILE REFERENCE: 4239-66642
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/530,340
 C--> 13 <141> CURRENT FILING DATE: 2005-04-01
 13 <150> PRIOR APPLICATION NUMBER: PCT/US03/31321
 14 <151> PRIOR FILING DATE: 2003-10-01
 16 <150> PRIOR APPLICATION NUMBER: 60/442,005
 17 <151> PRIOR FILING DATE: 2003-01-22
 19 <150> PRIOR APPLICATION NUMBER: 60/415,867
 20 <151> PRIOR FILING DATE: 2002-10-02
 22 <160> NUMBER OF SEQ ID NOS: 14
 24 <170> SOFTWARE: PatentIn version 3.2
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 1810
 28 <212> TYPE: DNA
 29 <213> ORGANISM: Rattus rattus
 32 <220> FEATURE:
 33 <221> NAME/KEY: misc_feature
 34 <222> LOCATION: (1705)..(1705)
 35 <223> OTHER INFORMATION: n is a, c, g, or t
 37 <400> SEQUENCE: 1
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 40 ccgaagttaa agaaagcaag taaacgtatg acctgtcata agcggataa aatccagaaa 120
 42 aagggttcgag aacatcatcg aaaattaagg aaggaagcta aaaagcgggg tcacaagaag 180
 44 cctaagaagg acccaggagt tccaaatagt gctcccttta aagaggctct tcttcgtgaa 240
 46 gctgagctaa ggaaacagca gcttgaagaa ctaaaacagc agcagaaact tgacaggcaa 300
 48 aaagaacaag aacgaaaaag aaaacttgaa attagccctg atgatgagca atctaattgtg 360
 50 gaaactcagg aggaatctga tgagcccaaa ataaagaaag ctaaatcagg caaacagaat 420
 52 ccaaagaagt tacattgtca ggaacttaaa aagggtgattg aagcctcaga catttgtgta 480
 54 gaagtttttg atgccagaga tcctcttggt tgcagggtgc ctcaagtaga agaagctgtt 540
 56 atccaaagtg gatgtaaaaa actagtactt gtattaaata agtcagatct agtaccaaaa 600
 58 gagaatctag agaactggct aacttacttg aataaggaat tgccaacagt ggtgttcaaa 660
 60 gcctcaacaa acttaaagaa cagaaagaag acattcaaga taaagaagaa agttgttcca 720
 62 ttccaaagta aactctgctg tggcaaggaa gcactgtgga agctccttgg aggttttcag 780
 64 cagtcctgtg gaaaaggagt tcagggttga gtggttggtt tcccaaatgt gggaaaaagc 840
 66 agcatcatta atagtttaaa acaagaaagg aattgcagtg ttggagtttc catgggactt 900
 68 acaaggagta tgcagattgt cccttttagc aaacagatca caatcataga tagtccgtgc 960
 70 ttcattatct caccttgtaa ctcccctgct gcacttgccc tccgaagtcc agcaagtatt 1020

(ps.6)

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72 gaagttctaa gaccattgga ggctgccagt gccatcctgt ctcaggctga tagtcaacag 1080
74 gtgggtgtaa aatatactgt cccgggggtat aaggattctc tggatttttt tactaaactt 1140
76 gctcagagaa gaggtctgca ccaaaaaggt ggaagcccaa atgtcgaaag tgctgctaag 1200
78 ctgctatggg ctgagtgga aggtgcctca ttaggttact actgccatcc ccctgcatcc 1260
80 tggaatcatt ctctctattt taatgagaat attacagcaa tcatgaagag gggctttaat 1320
82 ctagaagaac tagaaaagaa taatgcacac agcatacaag tcctcaaggg ccctcattta 1380
84 actaataaaa tccttttccg gtcttcgggc ctgacaaatg gaataactaga agaaaaggac 1440
86 atccccgaag agtcaccaaa acagacagaa gaccaacagg atggtgatga tcaagaacat 1500
88 gttactgggtg aaaaaaatgc agagatctca gatgtgactc ctgtagaaga gaccagggag 1560
90 atgtcacctg ggcaatcaac agcaagtaaa ccatctgaca gatcctttat cttggataaa 1620
92 atgagtgaag aagacgatgc ctatgacttt accacagatt atatatagcc ttctaaatgt 1680
W--> 94 tcaagtgtgc tctgtacagt gttntagat tgctttggta tgatataaag tgtaaatcct 1740
96 gtgaatatgt atcatgtttt aaattaaaaa caaataaaaa agtgtttgta taaaaaaaaa 1800
98 aaaaaaaaaa 1810

101 <210> SEQ ID NO: 2
102 <211> LENGTH: 538
103 <212> TYPE: PRT
104 <213> ORGANISM: Rattus rattus
106 <400> SEQUENCE: 2
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109 1 5 10 15
112 Lys Arg Tyr Lys Ile Gln Lys Lys Val Arg Glu His His Arg Lys Leu
113 20 25 30
116 Arg Lys Glu Ala Lys Lys Arg Gly His Lys Lys Pro Lys Lys Asp Pro
117 35 40 45
120 Gly Val Pro Asn Ser Ala Pro Phe Lys Glu Ala Leu Leu Arg Glu Ala
121 50 55 60
124 Glu Leu Arg Lys Gln Gln Leu Glu Glu Leu Lys Gln Gln Gln Lys Leu
125 65 70 75 80
128 Asp Arg Gln Lys Glu Gln Glu Arg Lys Arg Lys Leu Glu Ile Ser Pro
129 85 90 95
132 Asp Asp Glu Gln Ser Asn Val Glu Thr Gln Glu Glu Ser Asp Glu Pro
133 100 105 110
136 Lys Ile Lys Lys Ala Lys Ser Gly Lys Gln Asn Pro Lys Lys Leu His
137 115 120 125
140 Cys Gln Glu Leu Lys Lys Val Ile Glu Ala Ser Asp Ile Val Leu Glu
141 130 135 140
144 Val Leu Asp Ala Arg Asp Pro Leu Gly Cys Arg Cys Pro Gln Val Glu
145 145 150 155 160
148 Glu Ala Val Ile Gln Ser Gly Cys Lys Lys Leu Val Leu Val Leu Asn
149 165 170 175
152 Lys Ser Asp Leu Val Pro Lys Glu Asn Leu Glu Asn Trp Leu Thr Tyr
153 180 185 190
156 Leu Asn Lys Glu Leu Pro Thr Val Val Phe Lys Ala Ser Thr Asn Leu
157 195 200 205
160 Lys Asn Arg Lys Lys Thr Phe Lys Ile Lys Lys Lys Val Val Pro Phe
161 210 215 220
164 Gln Ser Lys Leu Cys Cys Gly Lys Glu Ala Leu Trp Lys Leu Leu Gly
165 225 230 235 240

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168 Gly Phe Gln Gln Ser Cys Gly Lys Gly Val Gln Val Gly Val Val Gly
169                245                250                255
172 Phe Pro Asn Val Gly Lys Ser Ser Ile Ile Asn Ser Leu Lys Gln Glu
173                260                265                270
176 Arg Ile Cys Ser Val Gly Val Ser Met Gly Leu Thr Arg Ser Met Gln
177                275                280                285
180 Ile Val Pro Leu Asp Lys Gln Ile Thr Ile Ile Asp Ser Pro Cys Phe
181                290                295                300
184 Ile Ile Ser Pro Cys Asn Ser Pro Ala Ala Leu Ala Leu Arg Ser Pro
185 305                310                315                320
188 Ala Ser Ile Glu Val Leu Arg Pro Leu Glu Ala Ala Ser Ala Ile Leu
189                325                330                335
192 Ser Gln Ala Asp Ser Gln Gln Val Val Leu Lys Tyr Thr Val Pro Gly
193                340                345                350
196 Tyr Lys Asp Ser Leu Asp Phe Phe Thr Lys Leu Ala Gln Arg Arg Gly
197                355                360                365
200 Leu His Gln Lys Gly Gly Ser Pro Asn Val Glu Ser Ala Ala Lys Leu
201                370                375                380
204 Leu Trp Ser Glu Trp Thr Gly Ala Ser Leu Gly Tyr Tyr Cys His Pro
205 385                390                395                400
208 Pro Ala Ser Trp Asn His Ser Pro His Phe Asn Glu Asn Ile Thr Ala
209                405                410                415
212 Ile Met Lys Arg Gly Phe Asn Leu Glu Glu Leu Glu Lys Asn Asn Ala
213                420                425                430
216 His Ser Ile Gln Val Leu Lys Gly Pro His Leu Thr Asn Lys Ile Leu
217                435                440                445
220 Phe Arg Ser Ser Gly Leu Thr Asn Gly Ile Leu Glu Glu Lys Asp Ile
221                450                455                460
224 Pro Glu Glu Ser Pro Lys Gln Thr Glu Asp Gln Gln Asp Gly Asp Asp
225 465                470                475                480
228 Gln Glu His Val Thr Gly Glu Lys Asn Ala Glu Ile Ser Asp Val Thr
229                485                490                495
232 Pro Val Glu Glu Thr Arg Glu Met Ser Pro Gly Gln Ser Thr Ala Ser
233                500                505                510
236 Lys Pro Ser Asp Arg Ser Phe Ile Leu Asp Lys Met Ser Glu Glu Asp
237                515                520                525
240 Asp Ala Tyr Asp Phe Thr Thr Asp Tyr Ile
241                530                535

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244 <210> SEQ ID NO: 3

245 <211> LENGTH: 1770

246 <212> TYPE: DNA

247 <213> ORGANISM: Mus musculus

249 <400> SEQUENCE: 3

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250 gaattcggca cgagggttga accgcagttc cagttcgcac gtggcgcccg agaagtcgtg      60
252 gtgatcccgga gacctcctct gtccttgaag cgtccgcggc caggatgaag aggcctaagt      120
254 taaagaaagc gagtaaacgt atgacctgcc ataagcgata taaaattcaa aaaaaggtcc      180
256 gagaacatca tcgaaaatta aggaaggaag ctaaaaaacg gggtcacaag aagcctagga      240
258 aggaccagg tggtccaaat agtgctccct ttaaagaggc tcttcttcgt gaagctgaac      300
260 taaggaaaca gcagcttgaa gaactaaaac agcagcagaa acttgatagg caaaaagagc      360

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262 aagaaaggaa aagaaaactt gaagttagcc ctggtgatga gcagtctaata gtggaaacta 420
264 gggaggaatc tgacgagccc aaaagaaaaga aagccaaagc aggcaaacag aatccaaaga 480
266 agttacattg ccaggaactt aaaaagggtga ttgaagcctc agacattgtg ttagaagttt 540
268 tggatgccag agatcctctt ggttgcaggt gtcctcagat agaagaagct gttatccaga 600
270 gtgggagtaa gaagctgata ctgtatttaa ataagtctga tctagtacca aaggagaatt 660
272 tggagaactg gctaaattat ttgaataaaag aattgccaac cgtggtgttc aaagcctcaa 720
274 caaacttaaa gaacagaaaag acattcaaga taaaaaaagaa gaaagtgtt ccattccaaa 780
276 gcaaaatctg ctgtggcaag gaagcccttt ggaagcttct tggagatttt cagcagtcct 840
278 gtggaaagga tattcaagtt ggagtgattg gtttcccaaa tgtggggaaa agcagtgta 900
280 ttaatagctt aaaacaagaa tggatttgca atgttgggat ttccatggga cttacaagga 960
282 gcatgcagat tgtcccttta gacaagcaga tcacaatcat agacagtcca tgcctaatta 1020
284 tctcaccttg taactcccc actgcacttg cccttcggag tccagcaagc attgaggaac 1080
286 taagaccgct ggaggctgcc agtgccattc tgtctcaggc tgataatgaa caggtggtgt 1140
288 taaaatatac tgtccctgag tataaggatt ctctgcattt ttttactaaa cttgctcaaa 1200
290 gaagaggtct gcaccaaaaa ggtggaagcc caaatgtgga aagtgtgtct aagctggtgt 1260
292 ggtctgagtg gacaggtgcc tcattaggtt actattgcca tccccctgca tcctggaatc 1320
294 attctctgca ttttaatgag aatattgcag cagtcatgaa gaagggcttt aatctagaag 1380
296 aactagaaaa gaataatgca cacagcatac aagtcctcaa gggccctcat ttaactaata 1440
298 gaatcctttt tccgtcttcg gccctgacaa atggaatact agacgagaag gacatagtcg 1500
300 aagagaccag ggagctgtca cctgagcaat caacagcagg taagccatct gacgggtcgt 1560
302 ctgccttgga tagagcgagt caagaggatg aaacctatga cttcaccaca gattatatat 1620
304 aaccgccaca cactaacgtg ctctctgtac gctgtgtagt ttagtgtatg atataaactg 1680
306 tacatcttgt aaatatgtat catgttataa attcaaaata aaatacaagt atttgcttgc 1740
308 aaaaaaaaaa aaaaaaaact cgactctaga 1770

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311 <210> SEQ ID NO: 4

312 <211> LENGTH: 538

313 <212> TYPE: PRT

314 <213> ORGANISM: Mus musculus

316 <400> SEQUENCE: 4

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318 Met Lys Arg Pro Lys Leu Lys Lys Ala Ser Lys Arg Met Thr Cys His
319 1 5 10 15
322 Lys Arg Tyr Lys Ile Gln Lys Lys Val Arg Glu His His Arg Lys Leu
323 20 25 30
326 Arg Lys Glu Ala Lys Lys Arg Gly His Lys Lys Pro Arg Lys Asp Pro
327 35 40 45
330 Gly Val Pro Asn Ser Ala Pro Phe Lys Glu Ala Leu Leu Arg Glu Ala
331 50 55 60
334 Glu Leu Arg Lys Gln Gln Leu Glu Glu Leu Lys Gln Gln Gln Lys Leu
335 65 70 75 80
338 Asp Arg Gln Lys Glu Gln Glu Arg Lys Arg Lys Leu Glu Val Ser Pro
339 85 90 95
342 Gly Asp Glu Gln Ser Asn Val Glu Thr Arg Glu Glu Ser Asp Glu Pro
343 100 105 110
346 Lys Arg Lys Lys Ala Lys Ala Gly Lys Gln Asn Pro Lys Lys Leu His
347 115 120 125
350 Cys Gln Glu Leu Lys Lys Val Ile Glu Ala Ser Asp Ile Val Leu Glu
351 130 135 140
354 Val Leu Asp Ala Arg Asp Pro Leu Gly Cys Arg Cys Pro Gln Ile Glu
355 145 150 155 160

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358 Glu Ala Val Ile Gln Ser Gly Ser Lys Lys Leu Ile Leu Val Leu Asn
359          165          170          175
362 Lys Ser Asp Leu Val Pro Lys Glu Asn Leu Glu Asn Trp Leu Asn Tyr
363          180          185          190
366 Leu Asn Lys Glu Leu Pro Thr Val Val Phe Lys Ala Ser Thr Asn Leu
367          195          200          205
370 Lys Asn Arg Lys Thr Phe Lys Ile Lys Lys Lys Lys Val Val Pro Phe
371          210          215          220
374 Gln Ser Lys Ile Cys Cys Gly Lys Glu Ala Leu Trp Lys Leu Leu Gly
375 225          230          235          240
378 Asp Phe Gln Gln Ser Cys Gly Lys Asp Ile Gln Val Gly Val Ile Gly
379          245          250          255
382 Phe Pro Asn Val Gly Lys Ser Ser Val Ile Asn Ser Leu Lys Gln Glu
383          260          265          270
386 Trp Ile Cys Asn Val Gly Ile Ser Met Gly Leu Thr Arg Ser Met Gln
387          275          280          285
390 Ile Val Pro Leu Asp Lys Gln Ile Thr Ile Ile Asp Ser Pro Cys Leu
391          290          295          300
394 Ile Ile Ser Pro Cys Asn Ser Pro Thr Ala Leu Ala Leu Arg Ser Pro
395 305          310          315          320
398 Ala Ser Ile Glu Glu Leu Arg Pro Leu Glu Ala Ala Ser Ala Ile Leu
399          325          330          335
402 Ser Gln Ala Asp Asn Glu Gln Val Val Leu Lys Tyr Thr Val Pro Glu
403          340          345          350
406 Tyr Lys Asp Ser Leu His Phe Phe Thr Lys Leu Ala Gln Arg Arg Gly
407          355          360          365
410 Leu His Gln Lys Gly Gly Ser Pro Asn Val Glu Ser Ala Ala Lys Leu
411          370          375          380
414 Val Trp Ser Glu Trp Thr Gly Ala Ser Leu Gly Tyr Tyr Cys His Pro
415 385          390          395          400
418 Pro Ala Ser Trp Asn His Ser Leu His Phe Asn Glu Asn Ile Ala Ala
419          405          410          415
422 Val Met Lys Lys Gly Phe Asn Leu Glu Glu Leu Glu Lys Asn Asn Ala
423          420          425          430
426 His Ser Ile Gln Val Leu Lys Gly Pro His Leu Thr Asn Arg Ile Leu
427          435          440          445
430 Phe Arg Ser Ser Gly Leu Thr Asn Gly Ile Leu Asp Glu Lys Asp Ile
431          450          455          460
434 Val Glu Glu Ser Pro Ser Gln Thr Glu Asp Gln Gln Asp Ala Asp Asp
435 465          470          475          480
438 Gln Glu Asn Gly Ser Gly Glu Arg Asn Ala Glu Ile Ser Asp Val Ala
439          485          490          495
442 Pro Val Glu Glu Thr Arg Glu Leu Ser Pro Glu Gln Ser Thr Ala Gly
443          500          505          510
446 Lys Pro Ser Asp Gly Ser Ser Ala Leu Asp Arg Ala Ser Gln Glu Asp
447          515          520          525
450 Glu Thr Tyr Asp Phe Thr Thr Asp Tyr Ile
451          530          535
454 <210> SEQ ID NO: 5

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/530,340

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Input Set : A:\Sequence Listing.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 1705 ✓
Seq#:7; N Pos. 22,23
Seq#:8; N Pos. 22,23
Seq#:9; N Pos. 22,23
Seq#:10; Xaa Pos. 39,45,70,86,88,94,95,97,98,99,100,105,106,108,109,110,111
Seq#:10; Xaa Pos. 112,113,114,115,116,117,121,126,130,143,161,165,166,170
Seq#:10; Xaa Pos. 174,176,190,193,196,205,209,210,212,213,214,216,218,219
Seq#:10; Xaa Pos. 220,222,224,225,226,227,230,232,233,235,239,246,249,250
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Seq#:10; Xaa Pos. 314,317,318,330,331,332,334,346,347,357,359,360,363,367
Seq#:10; Xaa Pos. 374,380,385,390,400,407,410,411,412,413,414,418,420,421
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Seq#:10; Xaa Pos. 515,516,517,518,519,520,523,524,525,527,528,530,531,534
Seq#:10; Xaa Pos. 535,536,537,540,541,545,549

VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:94 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:1680
L:631 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
L:649 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:667 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:1149 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:32
M:341 Repeated in SeqNo=10